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(54) Title: FUMONISIN-DETOXIFYING ENZYMES

(57) Abstract

Methods for identifying organisms capable of degrading fumonisin. Fumonisin can be incorporated into culture medium for selection of organisms resistant to fumonisin and/or capable of growing on fumonisin as a sole carbon source. Using this method, several organisms have been identified. These organisms can be used to isolate the enzyme and the gene responsible for conferring fumonisin-resistance. The gene can be cloned and inserted into a suitable expression vector so that the protein can be further characterized. Additionally, the DNA encoding for fumonisin-resistance can be used to transform plant cells normally susceptible to *Fusarium* or other toxin-producing fungus infection. Plants can be regenerated from the transformed plant cells. In this way, a transgenic plant can be produced with the capability of degrading fumonisin, as well as with the capability of producing the degrading enzymes. Methods for detoxification in grain processing and in animal feed and rumen microbes are also disclosed.

ACTATGGAT CATTGATTC CCTGGCCGAG TGGCGGGCGG ATAGTCGTTG 1
CGAAGCTGG CAGAAATAGC GTGGGAAGTC GCGGGATGTC AAGATGGGG 51
CCGAGGATG GTGTCGGGGA CGGTTGGCGC GTTTCCTGCA TGGCTTGCGT 101
TCATCGTTG CGTGTACTCT AGGGGGACCC TCCGGCCGCC CGGGGGCAAC 151
CGGGACGAT TTTCGCGTC CGAGGGCGGA TCTGGGCCAG GTCAGGGGC 201
TGGGGGGGA CGTGATGAGC TTTCGGGAA TACCTTATGC AGCGCGCGCG 251
GTGGCGGGC TGGCTTGGAA GGCGCCCAA CACGGCGGG CCTGGGGGGG 301
CGTTGCGCC CGACCCCGAT TTTCTCGGA CTGGCTTGGG GGGGCTATAC 351
TTCCCAAGGG CACCTCTGGG CGGGGGGTGA GGGAGGACTG TCTTTCACCT 401
AAGCTATGGG CGGCTTGGGG CCGTAAACCC GCGCGTAAAC CGGTGATGGT 451
CTGGGTCTGCG GGGGGGGCT TGGCGGGGA CACGGGGGCC ATGGCTTACT 501
ACGAGCGGA GGCGCTTGGG CGACGGGGCG TGTGCTGGT GACGTTAAC 551
TATGGAGCA ACATCTCTGG CTTTTTCGGG CTCCTCTGGG TCTGGGGGG 601
GAGGCGGCGG CGGACCTGGG CTGACCTACG CCTACTCGAC ATTCCTGGGG 651
CTCTGGCTG GTCGACAGAC AGCGGGCGG CCTTGCGGG CGACGGGGCG 701
CGAGTGAAC TCTTGGTGA ATCGGGCGGA CGAGGGCGGA TCGGACTTCT 751
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CACCTGATG CGGGGGCGGC ACGGGGCGCG CGGGGGCTGG CGGGGGCTGC 951
GCAGGGGGCG TCCGACCGGA CGGATGCTG ATGGCCATGT GTGCGGGCG 1001
ACGGACAGCC CGGGGATGCC CGGGGGGGCG CTGGGGCGCG TTGGGGCTCT 1051
GATGGGAGCC CGGGGGCGGC AGGGGGCGGC CTGGGGGGCG CGGGGGGGCG 1101
TGGGAGGGT CGGGGGCGAC AGGGGGCGGC CTGGCTGGCA GTTGGGGGAC 1151
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CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG TGGGGGGCG GGGGGGGGG 1651
TGACGACGGT CGGGGGGGTG TTGGGGATCT CGGGGGGGCG CGGGGGGGT 1701
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FUMONISIN-DETOXIFYING ENZYMES.

This is a continuation-in-part of prior copending U.S. application Serial No. 08/289,595, filed August 12, 1994.

5 **Technical Field**

The present invention relates generally to the detection and isolation of fumonisin resistant organisms and to compositions and methods for the *in vivo* detoxification or degradation of fumonisin. This method has broad application in agricultural biotechnology and crop agriculture and in the improvement of food grain quality.

10 **Background of the Invention**

Fungal diseases are common problems in crop agriculture. Many strides have been made against plant diseases as exemplified by the use of hybrid plants, pesticides and improved agricultural practices. However, as any grower or home gardener can attest, the problems of fungal plant disease continue to cause difficulties in plant cultivation. Thus, there is a 15 continuing need for new methods and materials for solving the problems caused by fungal diseases of plants. These problems can be met through a variety of approaches. For example, the infectious organisms can be controlled through the use of agents that are selectively biocidal for the pathogens. Another method is interference with the mechanism by which the pathogen invades the host crop plant. Yet another method, in the case of pathogens that cause 20 crop losses, is interference with the mechanism by which the pathogen causes injury to the host crop plant. Still another method, in the case of pathogens that produce toxins that are undesirable to mammals or other animals that feed on the crop plants, is interference with toxin production, storage, or activity. This invention falls into the latter two categories.

Since their discovery and structural elucidation in 1988 (Bezuidenhout S, Gelderblom 25 W, Gorst-Allman C, Horak R, Marasas W, Spiteller B, Vleggaar R (1988) "Structure elucidation of the fumonisins, mycotoxins from *Fusarium moniliforme*." *Journal Chem Soc, Chem Commun* 1988: 743-745), fumonisins have been recognized as a potentially serious problem in maize-fed livestock. They are linked to several animal toxicoses including 30 leukoencephalomalacia (Marasas WFO, Kellerman TS, Gelderblom WCA, Coetzer JAW, Thiel P (1988) "Leukoencephalomalacia in a horse induced by fumonisin B-1 isolated from *Fusarium moniliforme*." *Onderstepoort Journal of Veterinary Research* 55: 197-204; Wilson TM, Ledet AE, Owens DL, Rice LG, Nelson HA (1990) "Experimental liver

disease in ponies associated with the ingestion of a corn-based ration naturally contaminated with fumonisin B₁," **American Association of Veterinary Laboratory Diagnosticians: Abstracts 33rd Annual Meeting**, Denver, Colorado, October 7-9, 1990., Madison, Wisconsin, USA) and porcine pulmonary edema (Colvin BM, Harrison LR (1992) 5 "Fumonisin-Induced Pulmonary Edema and Hydrothorax in Swine." **Mycopathologia** 117: 79-82). and are also suspected carcinogens (Geary W (1971) **Coord Chem Rev** 7: 81; Gelderblom WCA, Kriek NPJ, Marasas WFO, Thiel PG (1991) "Toxicity and Carcinogenicity of the *Fusarium*-Moniliforme Metabolite, Fumonisin-B1, in Rats." **Carcinogenesis** 12: 1247-1251; Gelderblom WCA, Semple E, Marasas WFO, Farber E 10 (1992) "The Cancer-Initiating Potential of the Fumonisin-B Mycotoxins." **Carcinogenesis** 13: 433-437). *Fusarium* isolates in section *Liseola* produce fumonisins in culture at levels from 2 to >4000 ppm (Leslie J, Plattner R, Desjardins A, Klittich C (1992) "Fumonisin B1 production by strains from different mating populations of *Gibberella fujikoroi* (*Fusarium* section *Liseola*)." **Phytopathology** 82: 341-345). Isolates from maize (predominantly mating 15 population A) are among the highest producers (Leslie *et al.*, *supra*). Fumonisin levels detected in field-grown maize have fluctuated widely depending on location and growing season, but both preharvest and postharvest surveys of field maize have indicated that the potential for high levels of fumonisins exists (Murphy PA, Rice LG, Ross PF (1993) "Fumonisin-B1, Fumonisin-B2, and Fumonisin-B3 content of Iowa, Wisconsin, and Illinois 20 corn and corn screenings." **J Agr Food Chem** 41: 263-266). Surveys of food and feed products have also detected fumonisin (Holcomb M, Thompson HC Jr., Hankins LJ (1993) "Analysis of fumonisin B-1 in rodent feed by gradient elution HPLC using precolumn derivation with FMOC and fluorescence detection." **J Agr Food Chem** 41: 764-767; Hopmans EC, Murphy PA (1993) "Detection of Fumonisin-B(1), Fumonisin-B(2), and 25 Fumonisin-B(3) and hydrolyzed Fumonisin-B(1) in Corn-Containing foods." **J Agr Food Chem** 41: 1655-1658; Sydenham EW, Shephard GS, Thiel PG, Marasas WFO, Stockenstrom S (1991) "Fumonisin Contamination of Commercial Corn-Based Human Foodstuffs." **J Agr Food Chem** 39: 2014-2018). The etiology of *Fusarium* ear mold is poorly understood, although physical damage to the ear and certain environmental conditions 30 can contribute to its occurrence (Nelson PE (1992) "Taxonomy and Biology of *Fusarium moniliforme*." **Mycopathologia** 117: 29-36). *Fusarium* can be isolated from most field grown maize, even when no visible mold is present. The relationship between seedling infection and

stalk and ear diseases caused by *Fusarium* is not clear. Genetic resistance to visible kernel mold has been identified (Gendloff E, Rossman E, Casale W, Isleib T, Hart P (1986) "Components of resistance to *Fusarium* ear rot in field corn." *Phytopathology* 76: 684-688; Holley RN, Hamilton PB, Goodman MM (1989) "Evaluation of tropical maize germplasm for resistance to kernel colonization by *Fusarium moniliforme*." *Plant Dis* 73: 578-580), but the relationship to visible mold to fumonisin production has yet to be elucidated.

Fumonisins have been shown in *in vitro* mammalian cell studies to inhibit sphingolipid biosynthesis through inhibition of the enzyme sphinganine acyl transferase (Norred WP, Wang E, Yoo H, Riley RT, Merrill AH (1992) "In vitro toxicology of fumonisins and the mechanistic implications." *Mycopathologia* 117: 73-78; Wang E, Norred W, Bacon C, Riley R, Merrill A Jr. (1991) "Inhibition of sphingolipid biosynthesis by fumonisins: implications for diseases associated with *Fusarium moniliforme*." *J Biol Chem* 266: 14486; Yoo HS, Norred WP, Wang E, Merrill AH, Riley RT (1992) "Fumonisin Inhibition of *de Novo* Sphingolipid Biosynthesis and Cytotoxicity Are Correlated in LLC-PK1 Cells." *Toxicol Appl Pharmacol* 114: 9-15), resulting in the accumulation of the precursor sphinganine. It is likely that inhibition of this pathway accounts for at least some of fumonisin's toxicity, and support for this comes from measures of sphinganine:sphingosine ratios in animals fed purified fumonisin (Wang E, Ross PF, Wilson TM, Riley RT, Merrill AH (1992) "Increases in Serum Sphingosine and Sphinganine and Decreases in Complex Sphingolipids in Ponies Given Feed Containing Fumonisins, Mycotoxins Produced by *Fusarium moniliforme*." *J Nutr* 122: 1706-1716). Fumonisins also affect plant cell growth (Abbas HK, Boyette CD (1992) "Phytotoxicity of fumonisin B₁ on weed and crop species." *Weed Technol* 6: 548-552; Vanasch MAJ, Rijkenberg FHJ, Coutinho TA (1992) "Phytotoxicity of fumonisin B₁, moniliformin, and t-2 toxin to corn callus cultures." *Phytopathology* 82: 1330-1332; Vesonder RF, Peterson RE, Labeda D, Abbas HK (1992) "Comparative phytotoxicity of the fumonisins, AAL-Toxin and yeast sphingolipids in *Lemna minor* L. (Duckweed)." *Arch Environ Contam Toxicol* 23: 464-467). Kuti *et al.* "Effect of fumonisin B₁ on virulence of *Fusarium* species isolated from tomato plants." (Abstract, Annual Meeting American Phytopathological Society, Memphis, TN: APS Press 1993) reported on the ability of exogenously added fumonisins to accelerate disease development and increase sporulation of *Fusarium moniliforme* and *F. oxysporum* on tomato.

The toxicity of fumonisins and their potential widespread occurrence in food and makes it imperative to find detoxification or elimination strategies to remove the compound from the food chain.

Disclosure of the Invention

5 The present invention is based on the discovery of organisms with the ability to degrade the mycotoxin fumonisin. In a search for a biological means of detoxifying fumonisins, we have isolated from field-grown maize kernels several dematiaceous hyphomycetes capable of growing on fumonisin B₁ or B₂ (FB₁ or FB₂) as a sole carbon source, degrading it partially or completely in the process. One species, identified as *Exophiala spinifera*, a "black yeast", was recovered from maize seed from diverse locations in the 10 southeastern and south central U.S. A related species, *Rhinocladiella atrovirens*, was isolated from seed originating in both Iowa and Georgia. We also isolated a bacterium, believed to be a *Xanthomonas* or *Sphingomonas* species, designated isolate 2412.1, from a field-grown maize stalk sample from Johnston, Iowa. This bacterium also showed growth on FB₁ as a sole 15 carbon source, and since its taxonomy is not certain we have deposited the strain with the American Type Culture Collection (ATCC) and it is referred to herein by its ATCC deposit number, 55552. We have also deposited enzyme-active strains of *Exophiala spinifera* (ATCC 74269) and *Rhinocladiella atrovirens* (ATCC 74270).

20 All isolates showed the capability to degrade FB₁ in liquid culture. By "degrade" is simply meant that the enzyme is capable of using fumonisin as a substrate and converting it to a different chemical structure. However, our studies indicate that the resulting compounds are less toxic than the fumonisins themselves.

25 Overall, only 16 of 70 independent seed samples tested yielded degraders. However, several *E. spinifera* isolates, collected outside the U.S. from non-maize sources, were also found to metabolize fumonisins. Representative isolates of other *Exophiala* species tested (*E. jeanselmi*, *E. salmonis*, *E. piscifera*) did not degrade fumonisins, nor did non-maize 30 *Rhinocladiella* isolates, including *R. atrovirens* and *R. anceps*, nor fungi associated with ear molds including *Fusarium moniliforme*, *F. graminearum*, *Aspergillus flavus* and *Diplodia maydis*. Fumonisin-metabolizing black yeasts were found to possess an inducible hydrolyase activity that cleaves the tricarballylate esters of FB₁, as monitored by C₁₈-thin layer chromatography (TLC) and fluorescence detection of amines. The identity of the resulting amino alcohol compound, designated AP₁, was verified by FAB-mass spectroscopy. The latter

compound has utility as a chemical indicator of fumonisin metabolism. *E. spinifera* cultures further metabolized AP₁ to compounds of unknown identity that were not detectable by amine reagents on TLC. In sealed culture chambers, *E. spinifera* grown on ¹⁴C FB, as a sole carbon source, released ¹⁴CO₂ as detected in 1N KOH-saturated filter paper strips, totaling percent of added label in 48 hours. Heat-killed cultures similarly incubated did not release appreciable ¹⁴CO₂. Thus, at least a portion of the fumonisin is fully metabolized by this fungus. Crude, cell-free culture filtrates of the *E. spinifera* isolate designated 2141.10 contained a heat-labile, protease-sensitive hydrolase activity attributed to an enzyme tentatively characterized as an esterase with specificity for tricarballylate esters of fumonisins and similar molecules such as 5 AAL-toxin from *Alternaria alternata lycopersici*. This purified esterase is believed to be a new chemical entity, since no commercially available esterases tested were able to hydrolyze the tricarballylate esters of FB₁, suggesting a novel enzyme specificity produced by these fungi. Cell-free extracts of *E. spinifera* isolate 2141.10 also contain an AP₁ catabolase capable 10 of converting AP₁ to a compound lacking a free amine group, possibly an aldehyde. These enzymes and genes coding for these enzymes, being involved in fumonisin degradation, have 15 utility in detoxification of maize seed pre- or post-harvest.

Brief Description of the Drawings

FIGURE 1 is the nucleotide sequence including the open reading frame coding for the bacterial esterase gene (bases 94 to 1683).

20 FIGURE 2 is a hypothetical amino acid sequence of the polypeptide encoded by bases 94 to 1683 of the nucleotide sequence of FIGURE 1. Residues 1-38 represent the putative signal sequence. The polypeptide including the signal sequence has a calculated molecular weight of 55,026.68 (529 residues), with a calculated pI of 8.70. The polypeptide without the putative signal sequence has a calculated molecular weight of 51,495.63 (491 residues), with a 25 calculated pI of 8.19.

Detailed Description of the Invention

This invention provides newly discovered enzymes capable of degrading and detoxifying fumonisins, produced by fermentation of one or more of *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 55552.

30 The invention further comprises methods for making enzymes that are capable of detoxifying fumonisins, comprising the step of growing one or more of *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium ATCC 55552 in the presence of a

fumonisins or the metabolite produced by action of the enzyme on a fumonisins. This invention further provides methods of detoxifying fumonisins, comprising the step of reacting them with an enzyme derived from *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 55552.

5 We have isolated and sequenced the gene that codes for the fumonisin-degrading enzyme from one of these organisms and provide the amino acid sequence of the enzyme here. It is known that genes encoding desired proteins can be identified, isolated, cloned and expressed in transgenic organisms, including several important crop plants. One commonly used method of gene transfer in plants involves the use of a disarmed form of the Ti plasmid of the soil 10 bacterium *Agrobacterium tumefaciens*. *A. tumefaciens* is a plant pathogen that causes crown-gall tumors in infected plants. Large plasmids, termed Ti- or tumor-inducing plasmids, are responsible for the oncogenicity of the bacterium as well as for the transfer of foreign DNA to the plant. Similarly, *A. rhizogenes* contains Ri- or root-inducing plasmids that induce root 15 growth. Both plasmid types include a *vir* or virulence region that must be functional in order to transform wild-type cells to tumor cells.

Transformation results in the integration of another plasmid portion, termed the T- or transfer-DNA, into the nuclear genome of the transformed cells. Ri and Ti plasmids can be manipulated to allow insertion of foreign DNA, encoding a desired protein, into the T-DNA region. The foreign DNA can be transferred either via a vector bearing both the *vir* gene and 20 the foreign gene or by a binary vector system consisting of two plasmids, one containing the *vir* gene and the other carrying the foreign gene. See, e.g., U.S. Pat. No. 4,658,082. Transformed plant cells can then be regenerated to produce varieties bearing the inserted gene. The production of transgenic, fumonisin-resistant plants will provide a useful and novel 25 approach for the control of *Fusarium*-induced plant diseases.

30 This invention also provides a mechanism for selection of transformants: growth of plant cells in the presence of a *Fusarium* or its mycotoxin favors the survival of plant cells that have been transformed to express the coding sequence that codes for the enzyme of this invention and degrade the toxin. Thus, the coding sequence that codes for the enzyme of this invention can itself be used as a selectable marker, or as a scorable marker by measuring formation of the amino alcohol metabolite.

Another embodiment of the present invention is directed to a DNA construct comprising an expression cassette comprised of:

a) a DNA coding sequence for a polypeptide capable of degrading fumonisin; and

b) control sequences that are operably linked to the coding sequence whereby the coding sequence can be transcribed and translated in a host cell, and at least one of the DNA coding sequences or control sequences is heterologous to the host cell.

5 Preferred embodiments of the subject invention include a host cell stably transformed by a DNA construct as described above; and a method of producing a polypeptide of a recombinant gene comprising:

- a) providing a population of these host cells; and
- b) growing the population of cells under conditions whereby the polypeptide encoded 10 by the coding sequence of the expression cassette is expressed.

In yet another embodiment, the present invention is directed to a transgenic plant capable of degrading fumonisin. In another embodiment, the transgenic plant is a maize plant capable of degrading fumonisin.

15 Another embodiment of the subject invention comprises a method of conferring fumonisin-resistance to a plant substantially without such resistance comprising transferring to the plant an expressible gene encoding a polypeptide capable of degrading fumonisin.

Thus, DNA encoding a protein able to inactivate fumonisin can be isolated and cloned 20 in an appropriate vector and inserted into an organism normally sensitive to the *Fusarium* or its toxin. Organisms expressing the gene can be easily identified by their ability to degrade fumonisin. The protein capable of degrading fumonisin can be isolated and characterized using techniques well known in the art. Furthermore, the gene imparting fumonisin-resistance can be transferred into a suitable plasmid, such as into the T-DNA region of the Ti or Ri plasmid of the soil bacteria *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*, respectively. Plant tissue can be inoculated with the transformed bacteria. Additionally, plant 25 tissues which have been co-cultivated with *Agrobacterium* spp. can be incubated in the presence of fumonisin to select for fumonisin-degrading transgenic plants, i.e., the gene for fumonisin degradation can serve as a selectable marker. Thus, the inoculated tissue is regenerated to produce fumonisin-degrading transgenic plants.

30 Additionally, the present invention relates to ruminal microorganisms that have been genetically engineered with the genes imparting fumonisin resistance. These engineered ruminal microorganisms can then be added to feed for consumption by animals susceptible to fumonisin and structurally related mycotoxins.

Industrial Applicability

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of botany, microbiology, tissue culture, molecular biology, chemistry, biochemistry and recombinant DNA technology, which are within the skill of the art. Such 5 techniques are explained fully in the literature. See, e.g., J. H. Langenheim and K. V. Thimann, **Botany: Plant Biology and Its Relation to Human Affairs** (1982) John Wiley; **Cell Culture and Somatic Cell Genetics of Plants**, Vol. 1 (I. K. Vasil, ed. 1984); R. V. Stanier, J. L. Ingraham, M. L. Wheelis, and P. R. Painter, **The Microbial World**, (1986) 5th Ed., Prentice-Hall; O. D. Dhringra and J. B. Sinclair, **Basic Plant Pathology Methods**, (1985) 10 CRC Press; Maniatis, Fritsch & Sambrook, **Molecular Cloning: A Laboratory Manual** (1982); **DNA Cloning**, Vols. I and II (D. N. Glover ed. 1985); **Oligonucleotide Synthesis** (M. J. Gait ed. 1984); **Nucleic Acid Hybridization** (B. D. Hames & S. J. Higgins eds. 1984); and the series **Methods in Enzymology** (S. Colowick and N. Kaplan, eds., Academic Press, Inc.).

15 In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

By "microbe" is meant any microorganism (including both eucaryotic and procarotic microorganisms), such as fungi, yeasts, bacteria, actinomycetes, algae and protozoa, as well as other unicellular structures capable of growth in culture.

20 A "fumonisin-producing microbe" is any microbe capable of producing the mycotoxin fumonisin or analogs thereof. Such microbes are generally members of the fungal genus *Fusarium*, as well as recombinantly derived organisms which have been genetically altered to enable them to produce fumonisin or analogues thereof.

25 By "degrading fumonisin" is meant any modification to the fumonisin molecule which causes a decrease or loss in its toxic activity. Such a change can comprise cleavage of any of the various bonds, oxidation, reduction, the addition or deletion of a chemical moiety, or any other change that affects the activity of the molecule. In a preferred embodiment, the modification includes hydrolysis of the ester linkage in the molecule as a first step.

Furthermore, chemically altered fumonisin can be isolated from cultures of microbes 30 that produce an enzyme of this invention, such as by growing the organisms on media containing radioactively-labeled fumonisin, tracing the label, and isolating the degraded toxin for further study. The degraded fumonisin can be compared to the active compound for its

phytotoxicity or mammalian toxicity in known sensitive species, such as porcines and equines. Such toxicity assays are known in the art. For example, in plants a whole leaf bioassay can be used in which solutions of the active and inactive compound are applied to the leaves of sensitive plants. The leaves may be treated *in situ* or, alternatively, excised leaves may be used. The relative toxicity of the compounds can be estimated by grading the ensuing damage to the plant tissues and by measuring the size of lesions formed within a given time period. Other known assays can be performed at the cellular level, employing standard tissue culture methodologies e.g., using cell suspension cultures.

5 By "structurally related mycotoxin" is meant any mycotoxin having a chemical structure related to a fumonisin such as fumonisin B1, for example AAL toxin, fumonisin B2, fumonisin B3, fumonisin B4, fumonisin C1, fumonisin A1 and A2, and their analogs, as well as other mycotoxins having similar chemical structures that would be expected to be detoxified by activity of the fumonisin degradative enzymes elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacteria of ATCC 55552.

10 15 By "harvested grain" is meant any form of grain which has been somehow removed from the environment in which it was grown. For example, harvested grain could constitute ear corn, or corn kernels removed from the ear, or cut wheat stalks, or barley or rice kernels, or the like. Harvested grain may be in storage or may be being processed. "Processed grain" is grain that has been through some form of processing and will be used in the production of 20 food for human consumption or will be used as animal feed.

By "transgenic plant" is meant any plant or plant cell that has become transformed by the introduction, stable and heritable incorporation, into the subject plant or plant cell, of foreign DNA, i.e. DNA encoding for a protein not normally found within that plant species.

25 "Plantlet" refers to a plant sufficiently developed to have a shoot and a root that is asexually reproduced by cell culture.

"Explant" refers to a section or piece of tissue from any part of a plant for culturing.

By "hormone" is meant any plant growth regulator that affects the growth or differentiation of plant cells. Such hormones include cytokinins, auxins, and gibberellins, as well as other substances capable of affecting plant cells.

30 The term "callus" and its plural "calli", refer to an unorganized group of cells formed in response to cutting, severing, or other injury inflicted on plant tissue. Excised pieces of plant tissue and isolated cells can be induced to form callus under the appropriate culture conditions.

Callus can be maintained in culture for a considerable time by transferring or subculturing parts of the callus to fresh medium at regular intervals. The transfer of callus to liquid medium leads to dispersion of the tissue and the formation of a plant cell suspension culture. Callus can be induced to undergo organized development to form shoots and roots.

5 "Embryoid" refers to a structure similar in appearance to a plant zygotic embryo.

"Somatic hybrid" and "somatic hybridization" refers generally to stable combination of cellular material, be it protoplast/protoplast or protoplast/cytoplasm combinations, and includes cybrids and cybridization.

10 A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication in vivo; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

15 As used herein, the term "nucleotide sequence" means a DNA or RNA molecule or sequence, and can include, for example, a cDNA, genomic DNA, or a synthetic DNA sequence, a structural gene or a fragment thereof, or an mRNA sequence that encodes an active or functional polypeptide.

20 A DNA "coding sequence" is a DNA sequence which is transcribed and translated into a polypeptide in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eucaryotic mRNA, genomic DNA sequences from eucaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

25 A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at its 3' terminus by the translation start codon (ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription. Within the promoter sequence will be found a transcription initiation site, as well as protein binding domains responsible for the binding of RNA polymerase.

Eucaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory 5 domains, enhancers, and the like, which collectively provide for the transcription and translation of a coding sequence in a host cell.

A coding sequence is "operably linked to" or "under the control of" control sequences in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding 10 sequence.

A "host cell" is a cell which has been transformed, or is capable of undergoing transformation, by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated into 15 (covalently linked to) chromosomal DNA making up the genome of the transformed cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eucaryotic cells, a stably transformed cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability 20 of the eucaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the exogenous DNA.

A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth in vitro for many generations.

25 Two DNA, RNA or polypeptide sequences are "substantially homologous" when at least about 85% (preferably at least about 90%, and most preferably at least about 95%) of the nucleotides or amino acids match over a defined length of the molecule. DNA sequences that are substantially homologous can be identified in a Southern hybridization experiment under, for example, stringent conditions, as defined for that particular system. Defining appropriate 30 hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *supra*; *DNA Cloning, Vols. I & II, supra*; *Nucleic Acid Hybridization, supra*.

A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature. Thus, when the heterologous region encodes a bacterial gene, the gene will usually be flanked by DNA that does not flank the bacterial gene in the genome of the source 5 bacterium. Another example of a heterologous coding sequence is a construct where the coding sequence itself is not found in nature (e.g., synthetic sequences having codons different from the native gene). "Heterologous" DNA also refers to DNA not found within the host cell in nature. Allelic variation or naturally occurring mutational events do not give rise to a heterologous region of DNA, as these terms are used herein.

10 The term "polypeptide" as used herein is used in its broadest sense, i.e., any polymer of amino acids (dipeptide or greater) linked through peptide bonds. Thus, the term "polypeptide" includes proteins, oligopeptides, protein fragments, analogues, muteins, fusion proteins and the like. The term also encompasses amino acid polymers as described above that include additional non-amino acid moieties. Thus, the term "polypeptide" includes glycoproteins, 15 lipoproteins, phosphoproteins, metalloproteins, nucleoproteins, as well as other conjugated proteins. The term "polypeptide" contemplates polypeptides as defined above that are recombinantly produced, isolated from an appropriate source, or synthesized.

20 This invention can be better understood by reference to the following non-limiting examples. It will be appreciated by those skilled in the art that other embodiments of the invention may be practiced without departing from the spirit and the scope of the invention as herein disclosed and claimed.

Example 1

25 **Chemicals and reagents.** All chemicals were reagent grade or better unless otherwise indicated. Fumonisin B₁ and B₂ were obtained from Sigma Chemical Co. Partially purified fumonisins (eluate from C8 column) were obtained from Dr. Pat Murphy (Iowa State University). AAL-toxin (TA isomer) was a gift of Dr. David Gilchrist (University of California-Davis).

30 **Plant tissue samples.** Mature, field-grown maize seed was obtained from maize breeding locations of Pioneer Hi-Bred International, Inc. in the Southeast, Midwest and South Central regions of the U.S. Seed was stored at room temperature in individual packets.

Fungal and bacterial isolates. *Exophiala* and *Rhinocladiella* isolates from maize were isolated as described below. Other isolates were obtained from Dr. C.J. Wang (Syracuse,

NY), Dr. Michael McGinnis (Case Western Reserve University, Cleveland, OH), and from the American Type Culture Collection (Bethesda, MD). *Fusarium graminearum* [*Gibberella zeae* (Schw.) Petsch], *Diplodia maydis*, and *Fusarium moniliforme* Shield., were obtained from the microbial culture collection of Pioneer Hi-Bred International, Inc.. *Aspergillus flavus* 5 (Schw.) Petsch, isolate CP22, was obtained from Don Sumner at the University of Georgia (Tifton, GA). *Xanthomonas* sp. 2412.1 was isolated from maize stalk tissue as described below.

Isolation methods. Individual kernels, either intact or split in two with a sterile razor blade, were rinsed for 1 hr in 5 ml sterile water with agitation. From 1 to 5 μ l of the rinse 10 fluid was added to 100 μ L of sterile, carbon-free mineral salts medium + FB₁ (MS-FB₁) (1 g/liter NH₃SO₄, 1 g/liter K₂HPO₄, 1 g/liter NaCl, 0.2 g/liter MgSO₄·7H₂O, pH 7.0) containing FB₁ (Sigma Chemical Co.) at 0.5 to 1.0 mg/ml). The pH of the medium was approx. 6.0 after addition of FB₁. After 1 to 2 weeks incubation at 28°C in the dark, serial 10-fold dilutions 15 were made in sterile dH₂O, and aliquots were plated onto 1.2% Bacto-agar containing 0.1% yeast extract, 1% Bacto-peptone and 0.1% dextrose (YPD agar). Fungal and bacterial colonies that appeared on agar were transferred onto fresh plates and individual colonies were evaluated for fumonisin metabolizing ability by inoculating them into fresh MS-FB₁. Loss of fumonisin from the medium was monitored periodically by spotting 0.5 to 1 microliter aliquots 20 of culture supernatant on C₁₈ silica gel plates that were then air-dried and developed as described below (see **Analysis of fumonisins and metabolism products**).

Direct isolation of black yeasts from seed was accomplished by plating 100 microliters of seed wash fluid onto YPD or Sabouraud agar augmented with cycloheximide (500 mg/liter) and chloramphenicol (50 mg/liter). Plates were incubated at room temperature for 7-14 days, and individual pigmented colonies that arose were counted and cultured for analysis of 25 fumonisin-degrading ability as described above.

For stalk isolations, mature stalk samples 0.5 x 0.5 x 2 cm were taken from Southern-type maize inbreds grown in Johnston, Iowa by Pioneer Hi-Bred International, Inc., a seed company, in 1993. One-inch sections of the center (pith) or the outside of non-surface-sterilized stalk were cut and placed in 10 ml. sterile water in a small, sterilized tube. The tubes 30 were shaken for 1 hour, and then 2 μ l of washate were withdrawn and used to inoculate 100 μ l of MS-FB₁ in a microtiter plate. Subsequent steps were as above.

Analysis of fumonisins and metabolism products. Analytical thin-layer chromatography was carried out on 100% silanized C₁₈ silica plates (SigmaTM #T-7020; 10 x 10 cm; 0.1 mm thick) by a modification of the published method of Rottinghaus. Sample lanes were pre-wet with methanol to facilitate sample application. After application of from 0.1 to 2 ⁵ µl of aqueous sample, the plates were air-dried and developed in MeOH:4% KCl (3:2) or MeOH:0.2 M KOH (3:2) and then sprayed successively with 0.1 M sodium borate (pH 9.5) and fluorescamine (0.4 mg/ml in acetonitrile). Plates were air-dried and viewed under long wave UV.

Alkaline hydrolysis of FB₁ to AP₁. FB₁ or crude fumonisin C₈ material was ¹⁰ suspended in water at 10-100 mg/ml and added to an equal volume of 4 N NaOH in a screw-cap tube. The tube was sealed and incubated at 60°C for 1 hr. The hydrolysate was cooled to RT and mixed with an equal volume of ethyl acetate, centrifuged at 1000 RCF for 5 minute and the organic (upper) layer recovered. The pooled ethyl acetate layers from two successive extractions were dried under N₂ and resuspended in dH₂O. The resulting material (the ¹⁵ aminopentol of FB₁ or "AP₁") was analyzed by TLC.

Tables 1 and 2 illustrate the results of efforts to isolate a fumonisin-degrading enzyme from a wide assortment of sources. As is noted, *E. spinifera* isolates from maize seed from various locations were always able to produce a fumonisin-degrading enzyme when grown on fumonisin as a sole carbon source (Table 1), as were *E. spinifera* isolates from other sources ²⁰ from around the world (Table 2). Some samples of *Rhinocladiella atrovirens* from maize seed were also able to produce this enzyme (Table 1). Other species of *Exophiala* and other sources and species of *Rhinocladiella* were routinely unable to produce the enzyme, even when isolated from plant-related sources (Table 2).

Table 1: Dematiaceous fungi isolated from maize seed that degrade fumonisin

Isolate#	Species	Location of origin	Isolated from	Appearance ¹	Modification of substrates	
					FB ₁	AP ₁
2369.E7	<i>Exophiala spinifera</i>	Tifton, GA	Maize seed (3293)	clean	+	+
2369.G5	<i>Exophiala spinifera</i>	Tifton, GA	Maize seed (3379)	clean	+	+
2174.A4	<i>Exophiala spinifera</i>	Tifton, GA	Maize seed (inbred)	moldy	+	+

Isolate#	Species	Location of origin	Isolated from	Appear- ance ¹	Modification of substrates	
					FB ₁	AP ₁
2369.F7	<i>Exophiala spinifera</i>	Winterville, NC	Maize seed (3170)	moldy	+	+
2369.H9	<i>Exophiala spinifera</i>	Winterville, NC	Maize seed (3379)	moldy	+	+
2141.10	<i>Exophiala spinifera</i>	Winterville, NC	Maize seed (unk)	moldy	+	+
2174.C6	<i>Rhino- cladiella atrovirens</i>	Winterville, NC	Maize seed (unk)	moldy	+	+
2170.2	<i>Exophiala spinifera</i>	Winterville, NC	Maize seed (inbred)	moldy	+	+
2174.A4	<i>Exophiala spinifera</i>	Union City, TN	Maize seed (inbred)	moldy?	+	+
2219.H5	<i>Exophiala spinifera</i>	Union City, TN	Maize seed (inbred)	moldy	+	+
2363.1	<i>Exophiala spinifera</i>	Weslaco, TX	Maize seed (inbred)	moldy	+	+
2363.3	<i>Exophiala spinifera</i>	Weslaco, TX	Maize seed (inbred)	moldy	+	+
2363.3	<i>Exophiala spinifera</i>	Weslaco, TX	Maize seed (inbred)	moldy	+	+
2363.8	<i>Exophiala spinifera</i>	Weslaco, TX	Maize seed (inbred)	moldy	+	+
2363.10	<i>Exophiala spinifera</i>	Weslaco, TX	Maize seed (inbred)	moldy	nt	
2369.F11	<i>Rhino- cladiella atrovirens</i>	Johnston, IA	Maize seed (inbred)	clean	+	+

¹ "moldy" implies visible discoloration of kernel pericarp, cracking or splitting; "clean" implies no visible signs of infection on the kernel

² Evaluated by TLC analysis of culture supernatants as described herein

nt = not tested.

Table 2: Other fungal isolates tested for degradation of fumonisin B1 in liquid culture

Isolate	Species	Source	Location of Origin	Isolated from	Modification of substrates	
					FB ₁	AP ₁
-Black Yeast Fungi -						
26089	<i>Exophiala spinifera</i>	ATCC	Uruguay	Palm trunk	+	+
26090	<i>Exophiala spinifera</i>	ATCC	Uruguay	Palm tree fruit	+	+
26091	<i>Exophiala spinifera</i>	ATCC	Uruguay	Bird's nest	+	+
26092	<i>Exophiala spinifera</i>	ATCC	Uruguay	Bird's nest	+	+
48173	<i>Exophiala spinifera</i>	ATCC		Nasal	+	+
				Granuloma		
56567	<i>Exophiala spinifera</i>	ATCC		?	+	+
18218	<i>Exophiala spinifera</i>	ATCC		Nasal	+	+
				Granuloma		
58092	<i>Exophiala spinifera</i>	ATCC		Human	+	+
66775	<i>Exophiala monileae</i>	ATCC			-	nt
32288	<i>Exophiala salmonis</i>	ATCC	Unknown	Leaf Litter	-	nt
26438	<i>Exophiala pisciphila</i>	ATCC	Australia	Wheat	-	nt
				rhizosphere		
26272	<i>Exophiala jeanselmi</i>	ATCC	Canada	Activated sludge	-	nt
P-154	<i>Rhinocladiella atrovirens</i>	C.J. Wang	Chester, NJ	Southern pine pole	-	nt
P-330	<i>Rhinocladiella atrovirens</i>	C.J. Wang	Binghamton, NY	Southern pine pole	-	nt
P-646	<i>Rhinocladiella atrovirens</i>	C.J. Wang	Virginia	Southern pine pole	-	nt
P-1492	<i>Rhinocladiella atrovirens</i>	C.J. Wang	Chester, NJ	Southern pine pole	-	nt

Isolate	Species	Source	Location of Origin	Isolated from	Modification of substrates	
					FB ₁	AP ₁
ED-43	<i>Rhinocladiella atrovirens</i>	C.J.	Unknown	Douglas-fir pole	-	nt
ED-124	<i>Rhinocladiella atrovirens</i>	C.J.	Unknown	Douglas-fir pole	-	nt
28220	<i>Rhinocladiella anceps</i>	ATCC	Maryland	Grass	-	nt
-Ear mold fungi -						
FMC001	<i>Fusarium moniliforme</i>	PHI	Unknown	Maize	-	nt
FGR001	<i>Fusarium graminearum</i>	PHI	Unknown	Maize	-	nt
CP22	<i>Aspergillus flavus</i>	PHI	Unknown	Maize	-	nt
DMA001	<i>Diplodia maydis</i>	PHI	Unknown	Maize	-	nt

*Tested both with FB₁ and as a sole carbon source and with FB₁ amended with 1% sucrose.

Table 3: Frequency of isolation of fumonisin-degrading black yeast isolates from maize seed

Location of origin	# samples tested	# samples positive	% containing FB ₁ -degrading black yeast	Species identified
Weslaco, TX	8	6	75.0	<i>Exophiala spinifera</i>
Winterville, NC	19	4	47.5	<i>Exophiala spinifera</i> , <i>Rhinocladiella atrovirens</i>
Tifton, GA	8	3	37.5	<i>Exophiala spinifera</i>
Union City, TN	7	2	28.2	<i>Exophiala spinifera</i>
Johnston, IA	7	1	14.3	<i>Rhinocladiella atrovirens</i>
Shelbyville, IL	3	0	0	none
Macomb, IL	4	0	0	-
Champaign, IL	3	0	0	-
Yale, IN	3	0	0	-
California	8	0	0	-
Total	70	16	22.8	

Organisms can be screened for their ability to degrade fumonisin using the present methods. In this way, plant, soil, marine and fresh water samples can be screened and organisms isolated therefrom that are able to degrade fumonisin. Alternatively, already isolated microbial strains that are suspected of possessing this capability can be screened.

Putative fumonisin-resistant bacteria include bacteria associated with plant species susceptible to *Fusarium* infection. For instance, bacteria associated with *Fusarium*-infected tomato and pepper as well as other susceptible plant species, might be expected to degrade fumonisin. Furthermore, members of bacterial genera known to be versatile in their catabolism of complex organic molecules, such as members of the genus *Pseudomonas*, might degrade fumonisin.

Generally, media used to culture the above microbes will contain a known amount of fumonisin, i.e. from 0.1 to 3 mg of fumonisin per ml of media, more usually from .25 to 2 mg per ml of media, and preferably from 0.5 to 1 mg of fumonisin per ml of media.

A further study was performed to determine if colony morphology could be used to determine which strains of these species would produce a fumonisin-degrading enzyme. The results as shown in Table 4 indicated that *E. spinifera* and *R. atrovirens* colonies having different morphologies could nevertheless produce the fumonisin-degrading enzyme.

Table 4: Black yeasts recovered from a single kernel by direct plating seed washates onto YPD + cycloheximide + chloramphenicol¹

Isolate	Colony Type on YPD agar	Species	# colonies	# FB ₁ degr
2403.5	Light brown, shiny	<i>Exophiala spinifera</i>	33	33
2403.25	Dark brown, shiny	<i>Exophiala spinifera</i>	1	1
2403.12	Brown, velvety	<i>Rhinocladiella atrovirens</i>	4	4
2403.2	Grey, velvety	<i>Rhinocladiella atrovirens</i>	1	1
Totals			39	39

Kernel source: Tifton, Georgia. Seed was split, washed in 5 ml sterile water and then 100 μ l was plated onto YPD agar containing cycloheximide (500 mg/L) and chloramphenicol (50 mg/L).

From these results it was concluded that growth on fumonisin as the sole carbon source is the most reliable indicator of the ability to produce the fumonisin-degrading esterase.

The esterase isolated from *E. spinifera* was then subjected to other treatments, including proteases, to determine whether and how the enzyme would function in various environments. The results are indicated in Table 5.

Table 5: Effect of various treatments on modification of FB₁

Treatment	Conditions	FB ₁ Hydrolase activity*
Control	16 hr, 37° C, pH 5.2	+++
Boiling water bath	100° C, 30 min, pH 5.2	-
Protease K	0.01 mg/ml, 16 hr, 37° C, pH 5.2	+
Pronase E	0.01 mg/ml, 16 hr, 37° C, pH 5.2	++
Chymotrypsin	0.01 mg/ml, 16 hr, 37° C, pH 5.2	++
Trypsin	0.01 mg/ml, 16 hr, 37° C, pH 5.2	+++
EDTA	50 mM	++
DTT	25 mM	+++
Ca ⁺⁺	50 mM	+++
Mg ⁺⁺	50 mM	+++
PMSF	10 mM	+++

* 10-fold concentrated, 11 to 15 day culture filtrates treated as described and then incubated with FB₁ (0.5 mg/ml final conc) overnight at 37°C. Analysis by C₁₈ TLC/fluorescamine spray following overnight incubation at 37°C with 1 mg/ml fumonisin

- = no hydrolysis
- 10 ± = trace amount of hydrolysis
- + = incomplete hydrolysis
- ++ = incomplete hydrolysis
- +++ = complete hydrolysis

Next, the pH range of activity of the fumonisin esterase was evaluated by measuring 15 fumonisin degradation in the presence of citrate and citrate-phosphate buffers at varying pH levels. Results are shown in Table 6. From this, it was concluded that the pH range of the enzyme was quite wide, and that the enzyme would function at the internal pH of plants and plant cells.

Table 6: Effect of buffer pH on hydrolysis of fumonisin B₁
by *E. spinifera* culture filtrate

Buffer	pH	FB ₁ Hydrolase activity*
0.1 M citrate	3.0	+++
0.1 M citrate-phosphate	4.0	+++
0.1 M citrate-phosphate	5.0	++
0.1 M citrate-phosphate	6.0	++
0.1 M phosphate	7.0	±
0.1 M phosphate	8.0	—

* reactions were carried out at 37°C overnight and then assayed by TLC

5 * Analysis by C₁₈ TLC/fluorescamine spray following overnight incubation at 37°C with 1 mg/ml fumonisin.

- = no hydrolysis
- ± = trace amount of hydrolysis
- + = incomplete hydrolysis
- 10 ++ = incomplete hydrolysis
- +++ = complete hydrolysis..

The fumonisin esterase isolated from *E. spinifera* and *R. atrovirens* was compared with other known esterases from various sources as supplied by commercial vendors. The results shown in Table 7 indicate that the fumonisin esterase is a unique enzyme that is highly specific in its activity and does not have a generalized esterase activity comparable to that of any of the known enzymes tested.

Table 7: Hydrolysis of fumonisin B₁ by commercial esterases and hydrolases

Enzyme	Code	Source, purity	Units/m	Units	Assay pH	FB ₁ hydrolysis
			g prot.	per rxn		
Esterase, nonspecific	EC 3.1.1.1	Rabbit	100		8.0	—
Esterase, nonspecific	EC 3.1.1.1	Porcine liver	200		7.5	—
Lipase	EC 3.1.1.3	Candida cylindrica	35		7.7	—
Cholinesterase, butyryl	EC 3.1.1.8	Horse serum, highly purified	500	15	8.0	—

Enzyme	Code	Source, purity	Units/m g prot.	Units per rxn	Assay pH	FB ₁ hydrolysis
Cholinesterase, acetyl	EC 3.1.1.7	Bovine, partially pure	0.33	0.15	8.0	—
Cholesterol esterase	EC 3.1.1.13	Bovine, partially pure	0.5	0.15	8.0	±
Cholesterol esterase	EC 3.1.1.13	Porcine, partially pure		0.15	8.0	—
Cholesterol esterase	EC 3.1.1.13	<i>Pseudomonas</i> <i>fluorescens</i>	12	1.5	7.0	—
Cholesterol esterase, 3.1.1.13	EC	<i>Pseudomonas</i> sp.	200	15	7.0	±
Acetylesterase	EC 3.1.1.6	Orange Peel partially pure	4	0.15	6.5	—
Pectinesterase	EC 3.1.1.11	Orange Peel, partially pure	100	1.5	7.5	—
Pectinase	EC 3.2.1.15	Rhizopus Crude	0.5	1.5	4.0	—
Pectinase	EC 3.2.1.15	<i>Aspergillus</i> Partially pure	5	0.1	4.0	—
Fumonisin esterase	?	<i>Exophiala</i> <i>spinifera</i> , crude	unk	unk	5.2	+++

* Analysis by C₁₈ TLC/fluorescamine spray following overnight incubation at 37° C with 1 mg/ml fumonisin.

— = no hydrolysis
 ± = trace amount of hydrolysis
 5 + = incomplete hydrolysis
 ++ = incomplete hydrolysis
 +++ = complete hydrolysis

The enzyme of this invention was evaluated for inducibility by growing an *Exophiala* culture on various carbon sources of varying degrees of structural similarity to fumonisin. The 10 results, shown in Table 8, illustrate that both the original form of fumonisin and its metabolite are capable of inducing enzyme production, but that inducibility of the enzyme is also quite specific.

Table 8: Ability of various carbon sources to support growth and/or induction of FB_1 hydrolytic activity
Exophiala culture activity

Carbon source	Concentration	Growth	FB_1 hydrolyase activity
FB_1	0.1%	+	+
Alkaline hydrolyzed FB_1 (API)	0.1%	+	+
Na+ Tricarballylate	0.1%	±	-
Sphingosine	0.1%	-	-
Phytosphingosine	0.1%	-	-
Na+ Citrate	0.1%	+	-
Sucrose	0.1%	+	-
Glucose	0.1%	+	-

5 The ability of the fumonisin esterase to cleave other organic carboxylesters was also evaluated in comparison to its ability to hydrolyse fumonisin. The results, shown in Table 8, also illustrate that the enzyme hydrolyzed the tricarballylates of other related aminoalcohols such as FB_2 and AAL toxin.

Table 9: Hydrolysis of organic carboxylesters by *Exophiala* crude concentrated culture filtrate

Substrate	Conditions	Assay method	Hydrolysis by <i>Exophiala</i> culture filtrate
FB_1	pH 5.2, 37° C, 1 hr	C_{18} TLC: fluorescamine	+
FB_2	pH 5.2, 37° C, 1 hr	C_{18} TLC: fluorescamine	+
AAL-toxin	pH 5.2, 37° C, 1 hr	C_{18} TLC: fluorescamine	+

10 **Enzyme activity of culture filtrate and mycelium.** *Exophiala spinifera* isolate 2141.10 was grown on YPD agar for 1 week, and conidia were harvested, suspended in sterile water, and used at 105 conidia per ml to inoculate sterile Fries mineral salts medium containing 1 mg/ml purified FB_1 (Sigma Chemical Co.). After 2 weeks incubation at 28°C in the dark, cultures were filtered through 0.45 micron cellulose acetate filters, and rinsed with Fries mineral salts. Fungal mycelium was suspended in 15 mL of 0.1 MC- FB_1 , pH 5.2 + 1 mM EDTA + 3 μ g/mL Pepstatin A + 1.5 μ g/mL Leupeptin and disrupted in a Bead Beater™ using 0.5 mm beads and one minute pulses, with ice cooling. Hyphal pieces were collected by

filtering through Spin X (0.22 μ m), and both mycelial supernatant and original culture filtrates were assayed for fumonisin modification by methods outlined above.

Preparation of crude culture filtrate. Agar cultures grown as above were used to inoculate YPD broth cultures (500 ml) in conical flasks at a final concentration of 10⁵ cells per ml culture. Cultures were incubated 5 days at 28°C without agitation and mycelia harvested by filtration through 0.45 micron filters under vacuum. The filtrate was discarded and the mycelial mat was washed and resuspended in sterile carbon-free, low mineral salts medium (1 g/liter NH₃NO₃; 1 g/liter NaH₂PO₄; 0.5 g/liter MgCl₂; 0.1 g/liter NaCl; 0.13 g/liter CaCl₂; 0.02 g/liter FeSO₄ · 7H₂O, pH 4.5) containing 0.5 mg/ml alkaline hydrolyzed crude FB₁. After 3-5 days at 28°C in the dark with no agitation the cultures were filtered through low protein binding 0.45 micron filters to recover the culture filtrate. Phenylmethyl sulfonyl fluoride (PMSF) was added to a concentration of 2.5 mM and the culture filtrate was concentrated using an Amicon™ YM10 membrane in a stirred cell at room temperature, and resuspended in 50 mM sodium acetate, pH 5.2 containing 10 mM CaCl₂. The crude culture filtrate (approx. 200-fold concentrated) was stored at -20°C.

To obtain preparative amounts of enzyme-hydrolyzed fumonisin, 10 mg. of FB₁ (Sigma) was dissolved in 20 mL of 50 mM sodium acetate at pH 5.2 + 10 mM CaCl₂, and 0.25 mL of 200x concentrated crude culture filtrate of 2141.10 was added. The solution was incubated at 37°C for 14 hours, and then cooled to room temperature. The reaction mixture was brought to approx. pH 9.5 by addition of 0.4 mL of 4 N KOH, and the mixture was extracted twice with 10 mL ethyl acetate. The combined organic layers were dried under LN₂ and resuspended in dH₂O. 2.5 milligrams of organic extracted material were analyzed by Fast Atom Bombardment (FAB) mass spectrometry. The resulting mass spectrum showed a major ion at M/2=406 mass units, indicating the major product of enzymatic hydrolysis was AP₁, which has a calculated molecular weight of 406.63.

Additional characterization of fumonisin esterases from *Exophiala spinifera* and Gram-negative bacterium species. Crude, concentrated culture filtrates (induced for FB₁ esterase activity) from *E. spinifera* isolate 2141.10 and *Xanthomonas* sp. 2412.1 were chromatographed on a Pharmacia® Superdex 75 size exclusion column and eluted with 50 mM sodium phosphate, pH 6.0 containing 0.2 M NaCl. One-mL fractions were collected and assayed for FB₁ esterase activity by methods described above. The retention times for the

2141.10 and 2412.1 FB₁ esterases resulted in estimated molecular weights of 44.5 and 28.7 kilodaltons, respectively.

Similarly, crude concentrated culture filtrates in 1.7 M ammonium sulfate were injected onto a Pharmacia® Phenyl Sepharose FPLC column equilibrated with 1.7 M ammonium sulfate in 50 mM sodium phosphate pH 6.0 (Buffer A). A 30 mL, linear gradient of Buffer A to distilled water was applied, followed by a wash with 0.1% Triton X-100 in 50 mM sodium phosphate, pH 6.0. One-mL fractions were collected and assayed for both FB₁ esterase and for nonspecific esterase (as measured by naphthyl acetate hydrolysis using the method of Dary et al. (1990) "Microplate adaptation of Gomori's assay for quantitative determination,"

10 **Journal of Economic Entomology** 83: 2187-2192. Figure 2a and b shows the retention times for the specific (i.e. FB₁) versus nonspecific (i.e. naphthyl acetate esterase) activities. Both fungal and bacterial FB₁ esterase activity eluted at approx. 0.4 M ammonium sulfate. Naphthyl acetate esterase activity was detected in both fungal and bacterial cultures but this activity did not co-elute with the FB₁ esterase activity. Thus the fungal and bacterial FB₁

15 esterases are not the same as nonspecific esterases detectable in the culture filtrates of these microbes.

Example 2

Cloning of genes coding for fumonisin esterase

Microorganisms demonstrating fumonisin-resistance can be used to create a genomic library using standard techniques, well known in the art. Thus, restriction enzymes can be used to render DNA fragments which can in turn be inserted into any number of suitable cloning vectors. Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. The cloning vector need only be capable of transforming a host cell incapable of fumonisin degradation. Examples of recombinant DNA vectors for cloning and host cells which they can transform, shown in parentheses, include the bacteriophage lambda (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFRI (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5 (*Saccharomyces*), and YCp19 (*Saccharomyces*). See, generally

20 **DNA Cloning**, Vols. I and II, *supra*, and Maniatis et al., *supra*. Particularly useful is a cloning

25 vector able to transform *E. coli*.

Once the cloning vector has been inserted into an appropriate host cell, the cells are grown on fumonisin containing media and screened for their ability to degrade fumonisin as previously described. Plasmid DNA inserts from colonies that degrade fumonisin are characterized by subcloning, transposon tagging, and DNA sequence analysis, all well within the skill in the art (see, e.g., Napoli, C., and Staskawicz, B. (1987) *J. Bact.* 169:572-578). Once a coding sequence is determined, recombinant protein molecules able to degrade fumonisin can be produced according to the present invention by constructing an expression cassette and transforming a host cell therewith to provide a cell line or culture capable of expressing the desired protein which is encoded within the expression cassette.

Sequences encoding the fumonisin degradation enzyme can be either prepared directly by synthetic methods based on the determined sequence, or by using the sequence to design oligonucleotide probes to clone the native coding sequence using known techniques. The oligonucleotide probes can be prepared and used to screen a DNA library from an organism able to degrade fumonisin as determined above. The basic strategies for preparing oligonucleotide probes and DNA libraries, as well as their screening by nucleic acid hybridization, are well known to those of ordinary skill in the art. See, e.g., **DNA Cloning**, Vol. I, *supra*; **Nucleic Acid Hybridization**, *supra*; **Oligonucleotide Synthesis**, *supra*; Maniatis et al., *supra*.

The coding sequence can be comprised entirely of the coding sequence so derived, or such sequences can be fused to other sequences (e.g., leader sequences) so that a fusion protein is encoded. See, e.g., U.S. Patents Nos. 4,431,739; 4,425,437 and 4,338,397, the disclosures of which are hereby incorporated by reference. Once an appropriate coding sequence for the fumonisin-degrading enzyme has been prepared or isolated, it can be cloned into any suitable vector or replicon, known in the art. These vectors are described above, with *E. coli* being the host bacterium particularly preferred.

To complete construction of the expression cassettes, the coding sequence is then operably linked to control sequences such as a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator, so that the DNA sequence encoding the protein is transcribed into messenger RNA in the host cell transformed by the vector containing the expression construction. It is within the skill of the art to operably link the fumonisin-degrading enzyme coding sequence to appropriate control sequences in order to bring about transcription and translation. In general, the coding sequence will be downstream from the

promoter sequence and any expression regulatory regions, such as enhancers or operator sequences. If the coding sequence is linked to a heterologous coding sequence or start codon, then it is important to place the coding sequence in reading frame with the latter. If the intended expression host is procaryotic, then it will also be necessary to include a ribosome binding site among the upstream control sequences. Downstream operably linked control sequences will usually comprise a transcription termination sequence.

5 The construct can then be inserted into an appropriate expression vector. A number of procaryotic and eucaryotic expression vectors are known in the art. Preferred vectors are procaryotic expression vectors. A particularly preferred host for such vectors is *E. coli*. The 10 fumonisin-degrading enzyme is then produced by growing the host cells transformed by the expression cassette under conditions which cause the expression of the biologically active protein, as indicated by the host cells ability to degrade fumonisin in the medium on which it is grown, as described above. The protein can be isolated from the host cells and purified for further study. If the protein is not secreted, it may be necessary to disrupt the host cells and 15 purify the protein from the cellular lysate. Various purification techniques, such as HPLC, size-exclusion chromatography, electrophoresis, and immunoaffinity chromatography, are known, and the selection of the appropriate purification and recovery method is within the skill of the art.

Similarly, the gene can be inserted into the T-DNA region of a Ti or Ri plasmid 20 derived from *A. tumefaciens* or *A. rhizogenes*, respectively. Thus, expression cassettes can be constructed as above, using these plasmids. Many control sequences are known which when coupled to a heterologous coding sequence and transformed into a host organism show fidelity in gene expression with respect to tissue/organ specificity of the original coding sequence. See, e.g., Benfey, P. N., and Chua, N. H. (1989) *Science* 244: 174-181. Particularly suitable 25 control sequences for use in these plasmids are promoters for constitutive leaf-specific expression of the gene in the various target plants. Other useful control sequences include a promoter and terminator from the nopaline synthase gene (NOS). The NOS promoter and terminator are present in the plasmid pARC2, available from the American Type Culture Collection and designated ATCC 67238. If such a system is used, the virulence (*vir*) gene 30 from either the Ti or Ri plasmid must also be present, either along with the T-DNA portion, or via a binary system where the *vir* gene is present on a separate vector. Such systems, vectors for use therein, and methods of transforming plant cells are described in U.S. Pat. No.

4,658,082; U.S. application Ser. No. 913,914, filed Oct. 1, 1986, as referenced in U.S. Patent 5,262,306, issued November 16, 1993 to Robeson, et al.; and Simpson, R. B., et al. (1986)

Plant Mol. Biol. 6: 403-415 (also referenced in the '306 patent); all incorporated by reference in their entirety.

5 Once constructed, these plasmids can be placed into *A. rhizogenes* or *A. tumefaciens* and these vectors used to transform cells of plant species which are ordinarily susceptible to *Fusarium* or *Alternaria* infection. For example, non-resistant varieties of tomato (*Lycopersicon esculentum*) are often plagued with such infection and new resistant varieties could be developed to withstand *Alternaria*-induced disease in emerging tomato seedlings, 10 although it should be noted that fusarium wilt in tomato is thought to be caused by *F. oxysporum*, not *F. moniliformis*, and *F. oxysporum* apparently does not produce fumonisin. Several other transgenic plants are also contemplated by the present invention including but not limited to soybean, corn, sorghum, alfalfa, rice, clover, cabbage, banana, coffee, celery, tobacco, cowpea, cotton, melon and pepper. The selection of either *A. tumefaciens* or *A. rhizogenes* will depend on the plant being transformed thereby. In general 15 *A. tumefaciens* is the preferred organism for transformation. Most dicotyledons, some gymnosperms, and a few monocotyledons (e.g. certain members of the *Liliales* and *Arales*) are susceptible to infection with *A. tumefaciens*. *A. rhizogenes* also has a wide host range, embracing most dicots and some gymnosperms, which includes members of the *Leguminosae*, 20 *Compositae* and *Chenopodiaceae*. Alternative techniques which have proven to be effective in genetically transforming plants include particle bombardment and electroporation. See e.g. Rhodes, C. A., et al. (1988) **Science** 240, 204-207; Shigekawa, K. and Dower, W. J. (1988) **BioTechniques** 6, 742-751; Sanford, J. C., et al. (1987) **Particulate Science & Technology** 5:27-37; and McCabe, D. E. (1988) **BioTechnology** 6:923-926.

25 Once transformed, these cells can be used to regenerate transgenic plants, capable of degrading fumonisin. For example, whole plants can be infected with these vectors by wounding the plant and then introducing the vector into the wound site. Any part of the plant can be wounded, including leaves, stems and roots. Alternatively, plant tissue, in the form of an explant, such as cotyledonary tissue or leaf disks, can be inoculated with these vectors and 30 cultured under conditions which promote plant regeneration. Roots or shoots transformed by inoculation of plant tissue with *A. rhizogenes* or *A. tumefaciens*, containing the gene coding for the fumonisin degradation enzyme, can be used as a source of plant tissue to regenerate

fumonisin-resistant transgenic plants, either via somatic embryogenesis or organogenesis. Examples of such methods for regenerating plant tissue are disclosed in Shahin, E. A. (1985) *Theor. Appl. Genet.* 69:235-240; U.S. Pat. No. 4,658,082; Simpson, R. B., et al. (1986) *Plant Mol. Biol.* 6: 403-415; and U.S. patent applications Ser. Nos. 913,913 and 913,914, 5 both filed Oct. 1, 1986, as referenced in U.S. Patent 5,262,306, issued November 16, 1993 to Robeson, et al.; the entire disclosures therein incorporated herein by reference.

Such transformed cells can also be used to regenerate transgenic plants capable of expressing, in specific tissues or constitutively, depending upon the type of promoter utilized, either the fumonisin degrading enzymes elaborated by *Exophiala spinifera*, ATCC 10 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 55552, or the AP₁ catabolase elaborated by those strains. Such transgenic plants can be harvested, and the appropriate tissues (seed, for example, if a seed specific promoter were used) can be subjected to large scale protein extraction and purification techniques, and the fumonisin degradation enzymes or AP₁ catabolases can be isolated for use in fumonisin and fumonisin hydrolysis 15 product detoxification processes.

Certain esterases fall into a family that is related by primary sequence and overall structure (Cygler M, Schrag JD, Sussman JL, Harel M, Silman I, Gentry MK, Doctor BP (1993) "Relationship between sequence conservation and 3-Dimensional structure in a large 20 family of esterases, lipases, and related proteins." *Protein Sci* 2: 366-382.). PCR primers were designed based on highly conserved regions of this esterase family and using these primers, a cDNA clone from *Exophiala spinifera* isolate 2141.10 was obtained that showed significant 25 homology to known esterases, and was specifically induced by fumonisin and other inducers. This esterase can be expressed in *E. coli* and its enzyme activity can be measured by means of the TLC assay described above. If no activity is obtained in *E. coli* then expression can be measured in yeast or another eukaryotic system.

Other methods can also be used to clone the gene. Purification of the protein and N-terminal sequencing allow design of specific DNA probes; generation of antibodies from purified protein and screening an expression library; using RNA enrichment methods to obtain cDNAs specific to the induced culture. Once the gene has been confirmed as corresponding to 30 fumonisin esterase, the cDNA clone can easily be ligated into appropriate expression vectors for expression of the enzyme in maize tissue culture cells, transgenic maize, and also in *Fusarium moniliforme* itself, that is useful for studying the mechanisms of pathogenesis.

associated with the fungus and its toxin. Transformed or transient-expressing maize tissue culture cells can then be evaluated for resistance to fumonisins relative to control transformed tissue, and in fact fumonisin can be used as a selection agent to isolate transformed cells from tissue culture.

5 **Cloning of *Xanthomonas/Sphingomonas* Esterase Gene:**

The *Xanthomonas* esterase gene was cloned in a lambda ZAP express expression library from Sau3A partially digested bacterial DNA (4-8 kb size selected from ATCC 55552). Pools of lambda lysates were tested for fumonisin esterase assay by TLC using pure fumonisin as a substrate, and positive pools were sub-sampled to enrich for positive clones. Individual 10 plaques were resuspended and activity assayed in the lysate. One positive clone was purified, phagemid excised and DNA prepared for sequencing. A 4 kilobase DNA fragment containing fumonisin esterase activity was sequenced and found to contain a 1589 base pair region containing a 529 amino acid open reading frame with high homology to members of the serine carboxylesterase type B superfamily. The open reading frame codes for a hypothetical protein 15 (called BEST1) with a putative signal peptide from amino acid 1 to 38, giving a mature protein with a calculated molecular weight of 51,495.63 daltons and a pI of 8.19. This open reading frame showed 52.5% similarity and 34% identity with the amino acid sequence of a rabbit cholinesterase (P37176). Other cholinesterases showed similar homology scores. The BEST1 sequence was also 53.0% similar and 36.4% identical to a *Bacillus subtilis* para-nitrobenzyl esterase (P04058). The open reading frame also showed 54.6% similarity and 34.9% identity with the *Exophiala spinifera* fumonisin esterase (Esp1). Aside from their 20 overall similarity with other type B carboxylesterases, Esp1 and BEST1 share two short amino acid domains not found in other known esterases of this type:

<u>Protein</u>	<u>Sequence</u>	<u>From</u>	<u>To</u>
ESP1	ATLM	292	295
BEST1	ATLM	286	289
ESP1	TNI	175	177
BEST1	TNI	172	174

25

These domains may be involved in the substrate specificity of these enzymes (Cygler M., Schrag, J.D., Sussman, J.L. Harel, M., Silman I., Gentry, M.K. Doctor, B.P. (1993)

Relationship between sequence conservation and 3-Dimensional structure in a large family of esterases, lipases, and related proteins. *Protein Sci.* 2:366-382.).

Example 3

Preparation of AP1-induced and non-induced mycelium.

5 *Exophiala spinifera* isolate 2141.10 was grown in YPD broth for 5 days at 28°C, mycelium was harvested on 0.5 micron cellulose acetate filters and transferred to fresh medium consisting of Fries mineral salts (Gilchrist DG, Grogan RG (1976) "Production and nature of a host-specific toxin from *Alternaria alternata* f.sp. *lycopersici*." *Phytopathology* 66: 165-171) amended with hydrolyzed fumonisin B1 (AP1) (0.5 mg/mL) or delta-10 aminobutyric acid (δ -ABA) (1 mg/mL) as the sole carbon source. Cultures were incubated in the dark for 48 hr at 28°C and culture supernatants removed by filtration through 0.5 micron cellulose acetate. The remaining mycelial mat was washed with sterile Fries mineral salts and then frozen in liquid nitrogen for storage.

Example 4

15 **RNA isolation from *Exophiala spinifera***

The mycelial mats described above (~1 gram) were ground in liquid nitrogen in a mortar and pestle following addition of 10 mL "TRIREAGENT" (Molecular Research Center, Inc. Cincinnati, OH) in the presence of 0.2 volume chloroform. The grindate was centrifuged and the resulting supernatant precipitated with isopropanol. The resulting pellet was extracted with phenol, ethanol precipitated, and stored at -80° C.

The RNA in water (0.4 mL) was enriched for poly-A-containing mRNA using biotin-oligo(dT) and a streptavidin magnetic bead system (Promega) using the manufacturer's instructions. The polyA(+) -enriched RNA was stored at -80° C.

First strand cDNA synthesis from polyA(+) -enriched RNA was carried out using M-25 MLV reverse transcriptase (37° C, 1 hr). The reaction mixture was extracted with phenol and chloroform. Aliquots were taken for polymerase chain reaction (PCR) using the degenerate primers identified in SEQUENCE I.D. NOS. 1 through 4.

ESP5'-OL1 GGGGAATTGARGAYTGNYTNTAYNTNAAYRT (SEQUENCE I.D. NO. 1)
30 ESP5'-OL2 GGGGAATTCMCNGTNNTNVNTGGATNYAYGGNGGNG (SEQUENCE I.D. NO. 2)

ESP3'-OL1 GGGAGCTTGGRTYNCCNCRAANKBNGCDATTT (SEQUENCE I.D. NO. 3)

ESP3'-OL2 GGGAGCTTCNCCNGCNSWYTCNCCRAANADNGTNA (SEQUENCE I.D. NO. 4)

5 Most bases designated "N" were inosines.

Thermocycler reaction conditions were:

1. 94° C 2 min
2. 94° C 30 sec
3. 45° C 2 min
- 10 4. 72° C 1 min
5. repeat steps 2-4 for 35 X
6. 72° C 5 min

The PCR reaction products were electrophoresed on horizontal agarose gels. Bands that were present only in induced lanes were excised and the DNA was eluted. The recovered 15 DNA was digested with HindIII and EcoRI and ligated into pBluescript SK+.

A recombinant clone from products amplified using ESP5'-OL2 and ESP3'-OL2 (ESP26-1) was recovered and sequenced. The cloned region contains an open reading frame with the partial protein or amino acid sequence

...SFHLYDGASFAANQDVIVVTINYRTNILGFPAAPQLPITQRNLGFLDQRFALDWVQR
20 NIAAFGGDPRKVT FFGESA... (SEQUENCE I.D. NO. 5)

The above deduced amino acid sequence from DNA fragment ESP26-1 showed significant homology to a family of proteins that includes cholinesterases, acetylcholinesterases, carboxylesterases, and certain lipases (Cygler M, Schrag JD, Sussman JL, Harel M, Silman I, Gentry MK, Doctor BP (1993) "Relationship between 25 sequence conservation and 3-Dimensional structure in a large family of esterases, lipases, and related proteins." Protein Sci 2: 366-382.)

Examples 5-6

Comparison of Deduced Amino Acid Sequence to Known Sequences

In comparison with a sequence published in Arpagaus, M., Chatonnet, A., Masson, P., 30 Newton, M., Vaughan, T.A., Bartels, C.F., Nogueira, C.P., La Du, B.N., and Lockridge, O. J. Biol. Chem. 266, 6966-6974 (1991), 43 of the 76 amino acids in ESP26-1 were identical to a dog pancreatic cholinesterase.

In another comparison 32 of 62 amino acids from ESP26-1 were identical to a fungal lipase, as published by Lotti, M., Grandori, R., Fusetti, F., Longhi, S., Brocca, S., Tramontano, A., and Alberghina, L., *Gene* 124, 45-55 (1993).

Example 7

5 **Northern blot analysis of induced, non-induced *Exophiala spinifera*:**

Total RNA extracted from *Exophiala spinifera* cultures as described in the preceding examples was electrophoresed on agarose gels containing formaldehyde, blotted to nitrocellulose, and probed with random-primed 32P-labelled ESP26-1 cDNA. The probe hybridized to an RNA of approximately 2.0 kilobases in size in the induced lane, but not in the 10 non-induced lane (see Figure 1).

Example 8

Isolation of full length cDNA of ESP26-1 from *Exophiala spinifera*.

To obtain 3'-end of the cDNA coding for the putative esterase, a 3'-rapid amplification of cDNA ends protocol (3'-RACE) was employed (Frohman, M.A., Dush, M.K., and Martin, 15 G.R. 1988 "Rapid production of full-length cDNAs from rare transcripts: Amplification using a single gene-specific oligonucleotide primer." *Proc. Natl. Acad. Sci.* 85: 8998-9002). 5 µg of total RNA isolated from AP1 induced *Exophiala spinifera* mycelia was used as template for reverse transcription reaction. The reverse transcription reaction and subsequent PCR 20 amplification was performed with a 3'-RACE kit (Gibco BRL). The gene-specific primer (ESP3'-1: GCTAGTTCGCAGCCAATCA-GGA) (SEQUENCE I.D. NO. 6) was designed based on ESP26-1 sequence.

PCR reaction conditions were:

1. 94° C 4 min
2. 94° C 45 sec
- 25 3. 60° C 25 sec
4. 72° C 3 min
5. repeat steps 2-4 for 40 X
6. 72° C 10 min

A resulting 1.5 kb DNA fragment was blotted to nitrocellulose and hybridized with 30 cDNA ESP26-1 under highly stringent hybridization and wash conditions (last wash: 0.1 X SSC, 0.5% SDS, 65°C for 30 min.) The DNA fragment was gel-isolated, ligated into a pGEM-T vector (Promega), and transformed into DH5α (Gibco BRL). The resulting plasmid

DNA (p3RC-2) was sequenced using M13 universal primer. Sequence comparison of 3RC-2 and ESP26-1 indicated the ESP26-1 overlapped 100% with the 5' end of 3RC-2 sequence.

To obtain the amino-terminal sequence, a 5'-RACE strategy was employed (Frohman, *et al.*, *supra*). 5 µg of total RNA isolated from AP1 induced *Exophiala spinifera*.mycelia was 5 reverse transcribed with SuperScript I RNase H- reverse Transcriptase (Gibco BRL) using an anti-sense primer constructed against ESP26-1 sequence (ESP5'-1:

AAAGGCTGCGATGTTCCGCTGTA) (SEQUENCE I.D. NO. 7). The cDNA was tailed with dATP using terminal transferase (Promega) and used as a template for nested amplification using a second gene-specific anti-sense primer (ESP5'-2:

10 TCGCTGTGTTATTGGCAGCTGAG. (SEQUENCE I.D. NO. 8). C was a silent mutation of A in order to create a Pvu II restriction site) and an end-blocked polyT primer (BamT17V: CGCGGATCCGTTTTTTTTTTTTTV) (SEQUENCE I.D. NO. 9).

PCR reaction conditions were:

1. 94° C 4 min
- 15 2. 94° C 45 sec
3. 40° C 45 sec
4. 60° C 25 sec
5. 72° C 3 min
6. repeat steps 2-5 for 41 X
- 20 7. 72° C 10 min

The PCR products were fractionated on a 1.5% agarose gel. The amplified product was gel-isolated, ligated into pGEM-T (Promega), and transformed into DH5 (Gibco BRL). The resulting 5' RACE product was sequenced and shown to overlap as expected with the 3' RACE product and to contain an open reading frame with significant homology to members of 25 the serine esterase/lipase superfamily described by Cygler *et al.* (*supra*). The overlapping sequences obtained by 3' RACE and 5' RACE were combined to yield a cDNA sequence corresponding to the complete open reading frame. The full length, 1937 bp cDNA clone from *Exophiala spinifera* 2141.10 (abbreviated ESP1) contains an open reading frame of 537 amino acids as shown below (SEQUENCE I.D. NO. 10).

30 MPSRYILSWLLTCFLGIAFGSRCGSSAPTVKIDAGMVVGTTTVPGTTATVSEFLGVPF
AASPTRFAPPTRPVPWSTPLQATAYGPACPQQFNYPEELREITMAWFNTPPPSAGESED
CLNLNIYVPGTENTNKAVMVWIYGGALEYGWNSFHLYDGASFAANQDVIVVTINYRT

NILGFP AAPQLPITQRNLGFLDQRFALDWVQRNIAFGGDPRKVTFQGSAGGRSVDV
LLTSMPHNPPFRAAIMESGVANYNFPKGDLSEPWNNTVQALNCTTSIDILSCMRRVDL
ATLMNTIEQLGLGFETYLDNVTVVYRSETARTGDIARVPVLVGTVANDGLLFVLGEN
DTQAYLEEAIPNQPDLYQTLLGAYPIGSPGIGSPQDQIAAIETEVRFQCPAIVAQDSRN
5 RGIPSWRYYYNATFENLELFPGSEVYHSSEVMVFGTYPVASATALEAQTSKYMQGA
WAAFAKNPMNGPGWKQVPNVAALGSPGKAIQVDVSPATIDQRCALYTHYYTELGTIA
PRTF

This open reading frame (ORF) shows some homology to members of the serine esterase/lipase superfamily described by Cygler et al. (supra). The most extensive homology is 10 35.9% identity in 320 amino acid overlap with butyrylcholinesterase from *Oryctolagus cuniculus* (rabbit).

The deduced Esp1 protein contains a putative signal peptide which is probably cleaved at position 26/27 yielding a mature protein with a calculated MW of 54953.781 and calculated pI of 4.5. These calculated values are consistent with the estimated MR and pI of 15 the fumonisin esterase activity described above.

A comparison of the Esp1 open reading frame consensus regions in the esterase superfamily (Cygler et al., *supra*) reveals numerous conserved features indicating Esp1 may code for a serine esterase. The Esp protein has a potential serine active site consensus at 223-228; a putative aspartate active site consensus at 335-341 that is typical of cholesterol esterases and *Drosophila* 6 and P proteins [the majority of members of this superfamily, including fungal lipases and carboxylesterases have glutamate at the active site instead of aspartate]; and a putative histidine active site that is different from any members of the family, containing additional amino acids between the G and H. The putative Esp mature protein has a total of 6 cysteines, for 3 possible disulfide bridges, consistent with at least a subset of the esterases in the superfamily described by Cygler et al., *supra*

25 Thus the Esp ORF has most of the hallmarks of a bona fide member of the lipase/esterase superfamily, including a putative active site triad and other conserved amino acids. The regions of conservation are not consistent with any one substrate subgroup (i.e. lipase, cholinesterase, carboxylesterase, or cholesterol esterase), but seem to be contain some 30 features of several of these, and Esp appears to be unique among known esterases in its putative active site His consensus sequence.

Example 9**Effect of FB₁ and AP₁ on maize coleoptiles**

Maize coleoptiles from 4 day dark-grown germinated maize seeds were excised above the growing point and placed in 96-well microtiter plates in the presence of 60 microliters of sterile distilled water containing FB₁ or AP₁ at approximately equimolar concentrations of 1.5, .5, .15, .05, .015, .005, .0015, or .0005 millimolar, along with water controls. After 2 days in the dark at 28° C the coleoptiles were placed in the light and incubated another 3 days. Injury or lack thereof was evaluated as follows:

	0	.0005	.0015	.005	.015	.05	.15	.5	1.5	mM
FB ₁	-	-	-	-	+-	+	+	+	+	
AP ₁	-	-	-	-	-	-	-	-	+	

+= brown necrotic discoloration of coleoptile

- = no symptoms (same as water control)

The results (see table above) indicate there is at least a 30-fold difference in toxicity between FB₁ and AP₁ to maize coleoptiles of this genotype. This is in general agreement with other studies where the toxicity of the two compounds was compared for plant tissues: In *Lemna* tissues, AP₁ was approx. 40-fold less toxic (Vesonder RF, Peterson RE, Labeda D, Abbas HK (1992) "Comparative phytotoxicity of the fumonisins, AAL-Toxin and yeast sphingolipids in *Lemna minor* L (Duckweed)." *Arch Environ Contam Toxicol* 23: 464-467.). Studies with both AAL toxin and FB₁ in tomato also indicate the hydrolyzed version of the molecule is much less toxic (Gilchrist DG, Ward B, Moussato V, Mirocha CJ (1992) "Genetic and Physiological Response to Fumonisin and AAL-Toxin by Intact Tissue of a Higher Plant." *Mycopathologia* 117: 57-64.). In a recent report Lamprecht *et al.* also observed an approximate 100-fold reduction in toxicity to tomato by AP₁ versus FB₁ (Lamprecht S, Marasas W, Alberts J, Cawood M, Gelderblom W, Shephard G, Thiel P, Calitz J (1994) Phytotoxicity of fumonisins and TA-toxin to corn and tomato. *Phytopathology* 84: 383391.)

Example 10**Effect of FB₁ and AP₁ on maize tissue cultured cells (Black Mexican Sweet, BMS)**

FB₁ or AP₁ at various concentrations was added to suspensions of BMS cells growing in liquid culture medium in 96-well polystyrene plates. After 1 week the cell density in wells was observed under low power magnification and growth of toxin-treated wells was compared to control wells that received water. Growth of BMS cells was significantly inhibited at 0.4

micromolar FB₁, but no inhibition was observed until 40 micromolar AP₁. This represents an approximate 100-fold difference in toxicity to maize tissue cultured cells. Similarly Van Asch et al. (Vanasch MAJ, Rijkenberg FHJ, Coutinho TA (1992) "Phytotoxicity of fumonisin b1, moniliformin, and t-2 toxin to corn callus cultures." *Phytopathology* 82: 1330-1332) 5 observed significant inhibition of maize callus grown on solid medium at 1.4 micromolar. AP₁ was not tested in that study, however.

Example 11

AP₁ Catabolase Activity

A cell-free extract that contains the catabolase activity was obtained by subjecting 10 substrate-induced *Exophiala spinifera* cells to disruption using a bead beater in sodium acetate buffer, pH 5.2, and recovering the cell-free supernatant by centrifugation and .45 micron filtration. Catabolic activity is assayed by incubating extracts with AP₁ (hydrolyzed fumonisin B₁ backbone) or ¹⁴C-labelled with the extract and evaluating by TLC on C18 silica. The product AP₁-N₁ has a lower R_f than AP₁ and is detected either by radiolabel scan or by H₂S0₄ 15 spray/charring of the TLC plate. AP₁-N₁ does not react with the amine reagent, fluorescamine, that is routinely used to detect AP₁ on TLC plates, suggesting that the amine group is missing or chemically modified. Activity is greater at 37°C than at room temperature, but following 30 min. at 65°C or 100°C (no AP₁ catabolic activity remained). Activity is maximal at pH to 9. At pH 9, complete conversion to AP₁-N₁ occurred in 30 minutes. 20 Activity is retained by 30,000 dalton molecular weight cutoff membrane, but only partially retained by 100,000 dalton molecular weight cutoff membrane. Other amine-containing substrates were tested for modification by the crude extract. fumonisin (with tricarboxylic acids attached) is not modified by the extract, indicating that hydrolysis must occur first for the catabolase to be active. Other long-chain bases (sphingosine, sphinganine, phytosphingosine) 25 are apparently not modified by the crude catabolase, suggesting the enzyme(s) is specific for the fumonisin backbone. Preparative amounts of the product, tentatively named AP₁-N₁, have also been purified and analyzed by C13 nmr. The results indicate that AP₁-N₁ lack an amino nitrogen, and that it probably contains a keto function. This may point to either an amine oxidase or an ammonia lyase enzyme. The product of either enzyme would not be expected to 30 display any significant toxicity (although this has not been tested).

Example 12**Demonstration of Functional Esterase Activity**

Demonstration of esterase activity was accomplished by expressing the *E. spinifera* cDNA in two heterologous systems (an insect cell/baculovirus expression system, and 5 transgenic maize obtained by microprojectile bombardment) and subsequently detecting fumonisin esterase activity in transformed tissue. Forty-four maize calli (Hi type II) were bombarded with the esterase gene fused to the ubiquitin promoter plus a selectable marker (PAT) plasmid. Using thin layer chromatographic analysis, 38 lines were positive for fumonisin hydrolysis based upon the presence of a free tricarboxylic acid spot in the TLC 10 plates. Four negative control calli had no such spot. Similar results were obtained with insect cells infected with a baculovirus expression vector containing the esterase clone.

Esterase activity was also detected in leaf tissue of regenerated T0 maize plants. Ten leaf punches (4mm dia) were taken from the 6th leaf of regenerated plants of roughly the same age (7 leaf stage) representing four classes of transformants: selectable marker (Bar) only, low 15 esterase (+), medium esterase (++) and high esterase (+++) expressors (based on callus data). Four plants, representing different events in each class, were sampled. The punches were suspended in 200 microliters of 50 mM sodium acetate buffer, pH 5.2, containing leupeptin and pepstatin to inhibit proteinases, and homogenized by rapid agitation with a 5/32" steel bead, twice for 30 sec. The homogenates were spun at 4000 rpm, 10 min. at 4C and 150 20 microliters supernatant recovered. Samples were assayed for protein concentration (Bradford assay) and adjusted to the same protein concentration and then assayed for fumonisin esterase activity using ¹⁴C-FB1 as a substrate. After 30 min. or 4 hrs. reactions were spotted on TLC plates (C18) and developed with MeOH:4%KC1 (3:2). Plates were scanned with a radiometric scanner (AMBIS) and scored for fumonisin esterase activity on a product), ++ (up 25 to 50% conversion to product) and +++ (between 90-100% conversion to product).

Results were as follows:

SAMPLE	CALLUS SCORE (30 MIN)	30 MIN. LEAF SCORE	4 HR. LEAF SCORE
A1	+	-	-
B1 Control	-	-	-
C1	++	-	-
D1	+	-	+
E1 Control	-	-	-
F1	+++	+	++
G1	+++	+	+++
H1	++	+	++
A2	+	-	-
B2 Control	-	-	-
C2 Control	-	-	-
D2	+++	+++	+++
E2	++	+	++
F2	-	-	-
G2	+++	+	+++
H2	+++	+	+++

In summary, 8 or 12 callus expressors were positive for leaf expression. All negative controls plus four callus expressors were negative. Of the four "+++" callus expressors, only one (D2) had the same high level (30 min. assay), but all were positive.

Example 13

Detoxification of Harvested Grain

The present invention also relates to a method of detoxifying a fumonisin or a structurally related mycotoxin with an enzyme having the structure of the fumonisin degradative enzymes or the AP₁ catabolase elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74210, or the bacterium of ATCC 55552 during the processing of grain for animal or human food consumption. Since the atmospheric ammoniation of corn has proven to be an ineffective method of detoxification (see B. Fitch Haumann, "Eradicating Mycotoxin in Food and Feeds," INFORM 6:248-257 (1995)), such a methodology is particularly critical where transgenic detoxification is not applicable.

In this embodiment, the fumonisin degradative enzyme and/or the AP₁ catabolase elaborated by *Exophiliala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74210, or the bacterium of ATCC 55552, are presented to grain during the processing procedure, at the appropriate stages of the procedure and in amounts effective for detoxification of fumonisins and structurally related mycotoxins. Detoxification by this method can occur not only during the grain processing, but also any time prior to feeding of the grain to an animal or incorporation of the grain into a human food product.

The enzymes can be introduced during processing in appropriate manners, for example as a wash or spray, or in dried or lyophilized form or powdered form, depending upon the nature of the milling process and/or the stage of processing at which the enzymatic treatment is carried out. See generally, Hoseney, R.C., Principles of Cereal Science and Technology, American Assn. of Cereal Chemists, Inc., 1990 (especially Chapters 5, 6 and 7); Jones, J.M., Food Safety, Eagan Press, St. Paul, MN, 1992 (especially Chapters 7 and 9); and Jelen, P., Introduction to Food Processing, Reston Publ. Co., Reston, VA, 1985. Processed grain to be used for animal feed can be treated with an effective amount of the enzymes in the form of an inoculant or probiotic additive, for example, or in any form recognized by those skilled in the art for use in animal feed. The enzymes of the present invention are expected to be particularly useful in detoxification during processing and/or in animal feed prior to its use, since the enzymes display relatively broad ranges of pH activity. The esterase from *Exophiliala spinifera*, ATCC 74269, showed a range of activity from about pH 3 to about pH 6, and the esterase from the bacterium of ATCC 55552 showed a range of activity from about pH 6 to about pH 9.

Example 14

Genetic Engineering of Ruminal Microorganisms

Ruminal microorganisms can be genetically engineered to contain and express either the fumonisin degrading enzymes or the AP₁ catabolase elaborated by *Exophiliala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552, or a combination of the enzymes. The genetic engineering of microorganisms is now an art recognized technique, and ruminal microorganisms so engineered can be added to feed in any art recognized manner, for example as a probiotic or inoculant. In addition, microorganisms capable of functioning as bioreactors can be engineered so as to be capable of mass producing either the fumonisin degrading enzymes or the AP₁ catabolase elaborated by *Exophiliala*

WO 96/06175

PCT/US95/10284

spinifera, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Duvick, Jon

Rood, Tracy A.

5 (ii) TITLE OF INVENTION: FUMONISIN DETOXIFICATION
COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pioneer Hi-Bred International

10 (B) STREET: 700 Capital Square, 400 Locust Street

(C) CITY: Des Moines

(D) STATE: IA

(E) COUNTRY: USA

(F) ZIP: 50309

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: Microsoft Windows 3.1 - Notepad

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

25 (A) NAME: Roth, Michael J.

(B) REGISTRATION NUMBER: 29,342

(C) REFERENCE/DOCKET NUMBER: 0272 US

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(A) TELEPHONE: 515-248-4895

30 (B) TELEFAX: 515-248-4934

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 bases

(B) TYPE: nucleotide

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: probe
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GGGGAATTG ARGAYTGNYT NTAYNTNAAY RT 32

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 bases
- (B) TYPE: nucleotide
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: probe
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGGAATTCM CNGTNNTNVT NTGGATNYAY GGNNGNG 37

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 bases
- 20 (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: probe
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAAGCTTG GRTYNCCNCC RAANKBNGCD ATRTT 35

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 36 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: probe
- 35 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAAGCTTC NCCNGCNSWY TCNCCRAANA DNGTNA

36

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 76 amino acid
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (partial)

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp

5 10 15

15 Val Ile Val Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe
20 25 30Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe
35 40 45Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
20 50 55 60Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Phe Phe Gly Glu Ser
65 70 75

Ala

(2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: probe

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTAGTTTCG CAGCCAATCA GGA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: nucleotide
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: probe
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
AAAGGCTGCG ATGTTCCGCT GTA 23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
15 (B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: probe
(iii) HYPOTHETICAL: NO
20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
TCGCTGTGTT ATTGGCAGCT GAG 23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 28 bases
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: probe
30 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
CGCGGGATCCG TTTTTTTTTT TTTTTTTV 28

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Pro Ser Arg Tyr Ile Leu Ser Trp Leu Leu Thr Cys Phe Leu
 5 10 15

10 Gly Ile Ala Phe Gly Ser Arg Cys Gly Ser Ser Ala Pro Thr Val
 20 25 30

Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro
 35 40 45

Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala
 15 50 55 60

Ala Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp
 65 70 75

Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln
 80 85 90

20 Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp
 95 100 105

Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu
 110 115 120

Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn Lys Ala
 25 125 130 135

Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp Asn
 140 145 150

Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
 155 160 165

30 Val Ile Val Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe
 170 175 180

Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe
 185 190 195

Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 200 205 210

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser

	215	220	225
	Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His		
	230	235	240
	Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn		
5	245	250	255
	Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr		
	260	265	270
	Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys		
	275	280	285
10	Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln		
	290	295	300
	Leu Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Val Val		
	305	310	315
	Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val		
15	320	325	330
	Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val		
	335	340	345
	Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro		
	350	355	360
20	Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile		
	365	370	375
	Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala Ile		
	380	385	390
	Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln		
25	395	400	405
	Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn		
	410	415	420
	Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr		
	425	430	435
30	His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala		
	440	445	450
	Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly		
	455	460	465
	Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp		
35	470	475	480

WO 96/06175

PCT/US95/10284

Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala
485 490 495
Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala
500 505 510
5 Leu Tyr Thr His Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
515 520 525
Thr Phe

WHAT IS CLAIMED IS:

1. A method of detoxifying a fumonisin or a structurally related mycotoxin, present in harvested grain, the method comprising reacting the fumonisin with an enzyme having the structure of the fumonisin degradative enzyme elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 55552.
- 5 2. The method of Claim 1 wherein the detoxification reaction occurs during storage of the harvested grain.
3. The method of Claim 1 wherein the detoxification reaction occurs during processing of the harvested grain.
- 10 4. The method of Claim 1 wherein the detoxification reaction occurs in processed grain which is to be used as animal feed.
5. A method of detoxifying a fumonisin, a structurally related mycotoxin, a fumonisin hydrolysis product, or a hydrolysis product of a structurally related mycotoxin, present in harvested grain, the method comprising reacting the hydrolysis product with an AP₁ catabolase elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 15 74270, or the bacterium of ATCC 55552.
6. The method of Claim 5 wherein the detoxification reaction occurs during storage of the harvested grain.
7. The method of Claim 5) wherein the detoxification reaction occurs during 20 processing of the harvested grain.
8. The method of Claim 5 wherein the detoxification reaction occurs in processed grain which is to be used as animal feed.
9. A method for detoxifying, in harvested grain, a fumonisin or a structurally 25 related mycotoxin and for detoxifying a fumonisin hydrolysis product or a hydrolysis product of a structurally related mycotoxin, the method comprising reacting the fumonisin with an enzyme having the structure of the fumonisin degradative enzyme elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 55552, and reacting the hydrolysis product with an AP₁ catabolase elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atrovirens*, ATCC 74270, or the bacterium of ATCC 30 55552.
10. The method of Claim 9 wherein the detoxification reaction occurs during storage of the harvested grain.

21. A genetically engineered ruminal microorganism comprising an expression vector capable of expressing proteins in microorganisms, said vector comprising a nucleotide sequence encoding the AP₁ catabolase elaborated by *Exophilia spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.
- 5 22. A probiotic composition comprising the genetically engineered microorganisms of Claim 21.
23. A feed inoculant composition comprising the genetically engineered microorganism of Claim 21.
- 10 24. A genetically engineered microorganism comprising an expression vector capable of expressing proteins in microorganisms, said vector comprising a nucleotide sequence encoding the AP₁ elaborated by *Exophilia spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.

FIGURE 1

ACTAGTGGAT CATTGCATTG	1
GCTGGCGGAC TGGCGCGCCG	
ATAGTCGTTG	
CGATGGTCGC GAGAATAAGC	51
GTGCGAAGTG GGAGGATGTG	
AAGATGGGGG	
CCAGGAGTAT GTGTGCGGGA	101
CGGTCGGAC GCTTCTGCAT	
TGGCTTGGCT	
TCATCGGTTG CCGTGA	151
ACTCT AGGGGGAGCC	
TCCGCCGCG GCGCGGCAAC	
CGCGACGGAT TTTCCGGTCC	201
GCAGGACCGA TCTGGGCCAG	
GTTCAAGGAC	
TGGCCGGGGA CGTGATGAGC	251
TTTCGCGGAA TACCTATGC	
AGCGCCGCG	
GTGGGCGGGC TGCCTGGAA	301
GCCGCCCCAA CACGCCCGC	
CCTGGGCGGG	
CGTTCGCCCC GCCACCCAAT	351
TTGGCTCCGA CTGCTTCGGC	
GCGGCCTATC	
TTCGCAAAGG CAGCCTCGCC	401
CCCAGCGTGA GCGAGGACTG	
TCTTTACCTC	
AACGTATGGG CGCCGTCAGG	451
CGCTAAACCC GGCCAGTACC	
CCGTCATGGT	
CTGGGTCTAC GGCGCGGGCT	501
TCGCCGGCGG CACGCCCGC	
ATGCCCTACT	
ACGACGGCGA GGCGCTTGCG	551
CGACAGGGCG TCGTCGTGGT	
GACGTTAAC	
TATCGGACGA ACATCCTGGG	601
CTTTTCGCC CATCCTGGTC	
TCTCGCGCGA	
GAGCCCCACC GGAACCTCGG	651
GCAACTACGG CCTACTCGAC	
ATTCTCGCCG	
CTCTCGGTG GGTGCAGAGC	701
AACGCCCGCG CCTTCGGAGG	
GGACCCCGGC	
CGAGTGACGG TCTTTGGTGA	751
ATCGGCCGGA GCGAGCGCGA	
TCGGACTTCT	
GCTCACCTCG CCGCTGAGCA	801
AGGGTCTCTT CCGTGGCGCT	
ATCCTCGAAA	
GTCCAGGGCT GACGCGACCG	851
CTCGCGACGC TCGCCGACAG	
CGCCGCCTCG	
GGCGAGCGCC TCGACGCCGA	901
TCTTCGCCGA CTGCGCTCGA	
CCGACCCAGC	
CACCTGATG GCGCGCGCCG	951
ACGCCGCCCG CCCGGCATCG	
CGGGACCTGC	
GCAGGCCGCG TCCGACCGGA	1001
CCGATCGTCG ATGGCCATGT	
GCTGCCGCAG	
ACCGACAGCG CGGCGATCGC	1051
GGCGGGGCAG CTGGCGCCGG	
TTCGGGTCCT	
GATCGGAACC AATGCCGACG	1101
AAGGCCGCGC CTTCTCGGG	
CGCGCGCCGA	
TGGAGACGCC AGCGGACTAC	1151
CAAGCCTATC TGGAGGCGCA	
GTTTGGCGAC	
CAAGCCGCCG CCGTGGCGGC	1201
GTGCTATCCC CTCGACGCC	
GGGCCACGCC	
CAAGGAAATG GTCGCGCGA	1251
TCTTCGCCGA CAATCAGTTC	
AATCGGGGGG	
TCTCGGCCTT CTCGGAAGCG	1301
CTTGTGCGCC AGGGCGCGCC	
CGTGTGGCGT	
TATCAGTTCA ACGGTAATAC	1351
CGAGGGTGGA AGAGCGCCGG	
CTACCCACGG	
AGCCGAAATT CCCTACGTT	1401
TCGGGGTGT	
CAAGCTCGAC GAGTTGGTC	
TGTTCGATTG GCGCCCGAG	1451
GGGCCACGC CCGCCGACCG	
TGCGCTGGGC	
CAACTGATGT CCTCCGCCCTG	1501
GGTCCGGTTC GCCAAGAATG	
GCGACCCCGC	
CGGGGACGCC CTTACCTGGC	1551
CTGCCTATTC TACGGGCAAG	
TCGACCATGA	
CATTGGTCC CGAGGGCCGC	1601
GCGGCGGTGG TGTCGCCGG	
ACCTTCCATC	
CCCCCTTGCG CGGATGGCGC	1651
CAAGGCGGGG TGACGCCGTC	
GACGATGGCG	
TGACGACGGT CGAGGCGATG	1701
TTCTCGATCT GGAGTCCGCG	
CCGCCTCGAT	
TTGCGTCGTC TCCGGCGCTC	1751
AGACGAACGC CCCAGTTCCA	
TCCACACAGT	

FIGURE 2

MGARSMCAGR FGRFCIGLAS SVAVTLGGAS AAGAATATDF PVRRTDLGQV	1
QGLAGDVMSE RGIPYAAPV GGLRWKPPQH ARPWAGVRPA TQFGSDCFG A	51
AYLRKGSLAP GVSEDCLYLN VWAPSGAKPG QYPVMVWVYQ GGFAGGTAAM	101
PYYDGEALAR QGVVVVTFNY RTNILGFFAH PGLSRESPTG TSGNYGLLDI	151
LAALRWVQSN ARAFGGDPGR VTVFGESAGA SAIGLLLTSP LSKGLFRGAI	201
LESPGLTRPL ATLADSAASG ERLDADLSRL RSTDPA TLMA RADAARPASR	251
DLRRPRPTGP IVDGHVLPQT DSAAIAAGQL APVRVLIGTN ADEGRAFLGR	301
APMETPADYQ AYLEAQFGDQ AAAVAACYPL DGRATPKEMV ARIFGDNQFN	351
RGVSAFSEAL VRQGAPVWRY QFNGNTEGGR APATHGAEIP YVFGVFKLDE	401
LGLFDWPPEG PTPADRALGQ LMSSAWVRFA KNGDPAGDAL TWPAYSTGKS	451
TMTFGPEGRA AVVSPGPSIP PCADGAKAG*	501

11. The method of Claim 9 wherein the detoxification reaction occurs during processing of the harvested grain.
12. The method of Claim 9 wherein the detoxification reaction occurs in processed grain which is to be used as animal feed.
- 5 13. A transgenic plant capable of expressing the fumonisin degradative enzyme elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.
- 10 14. A transgenic plant capable of expressing the AP₁ catabolase elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.
- 15 15. A method of producing the fumonisin degradative enzyme elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552, the method comprising producing a transgenic plant which expresses one or more of said fumonisin degradative enzymes and isolating and purifying the enzymes from the plant tissues expressing the enzymes.
- 20 16. A method of producing the AP₁ catabolase elaborated by *Exophiala spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552, the method comprising producing a transgenic plant which expresses one or more of said AP₁ catabolases and isolating and purifying the enzymes from the plant tissues expressing the enzymes.
- 25 17. A genetically engineered ruminal microorganism comprising an expression vector capable of expressing proteins in microorganisms, said vector comprising a nucleotide sequence encoding the fumonisin degradative enzyme elaborated by *Exophilia spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.
18. A probiotic composition comprising the genetically engineered microorganisms of Claim 17.
- 30 19. A feed inoculant composition comprising the genetically engineered microorganism of Claim 17.
20. A genetically engineered microorganism comprising an expression vector capable of expressing proteins in microorganisms, said vector comprising a nucleotide sequence encoding the fumonisin degradative enzyme elaborated by *Exophilia spinifera*, ATCC 74269, *Rhinocladiella atravirens*, ATCC 74270, or the bacterium of ATCC 55552.